

Amendments to the Specification

On page 15, please replace the description of Figure 3 with the following paragraph:

--FIG. 3 contains the nucleotide sequence (SEQ ID NO: 2) and deduced amino acid sequence (SEQ ID NO: 1) of the novel type α PDGF receptor encoded by the T11 gene.--

On page 76, please replace the description of Figure 3 with the following paragraph:

--Figure 3. T11 cDNA nucleotide (SEQ ID NO:2) and predicted amino acid sequences. Nucleotides are numbered at the left. The predicted amino acid sequence (SEQ ID NO:1) of the long open reading frame is shown above the nucleotide sequence. Amino acids are numbered over the amino acids, starting at the putative initiation codon. The potential N-terminal signal sequence is underlined. Potential sites of N-linked glycosylation are overlined, and cysteine residues are boxed. The putative single transmembrane region is indicated by a shaded bar. The potential ATP binding site in the kinase domain is indicated by circles over Gly at residues 600, 602 and 605 and Lys at residue 627. The putative tyrosine autophosphorylation site at residue 849 is indicated by *. The regions of the λ T11 genomic sequence defined by exons a, b and c are underlined. The AATAAA box close to the polyadenylated 3' end of the cDNA is underlined as well.--